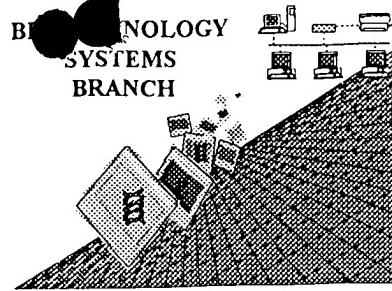


F LU

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#9
JLB

RAW SEQUENCE LISTING ERROR REPORT

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) detected errors when processing the following computer readable form:

MAY - 1 2001

RECEIVED

TECH CENTER 1600/2900

Application Serial Number: 09/397, 957
Source: 1655
Date Processed by STIC: 4-17-01

THE ATTACHED PRINTOUT EXPLAINS DETECTED ERRORS.

PLEASE FORWARD THIS INFORMATION TO THE APPLICANT BY EITHER:

- 1) INCLUDING A COPY OF THIS PRINTOUT IN YOUR NEXT COMMUNICATION TO THE APPLICANT, WITH A NOTICE TO COMPLY or,
- 2) TELEPHONING APPLICANT AND FAXING A COPY OF THIS PRINTOUT, WITH A NOTICE TO COMPLY

FOR CRF SUBMISSION QUESTIONS, PLEASE CONTACT MARK SPENCER, 703-308-4212.

FOR SEQUENCE RULES INTERPRETATION, PLEASE CONTACT ROBERT WAX, 703-308-4216.

PATENTIN 2.1 e-mail help: patin21help@uspto.gov or phone 703-306-4119 (R. Wax)

PATENTIN 3.0 e-mail help: patin3help@uspto.gov or phone 703-306-4119 (R. Wax)

TO REDUCE ERRORED SEQUENCE LISTINGS, PLEASE USE THE CHECKER VERSION 3.0 PROGRAM, ACCESSIBLE THROUGH THE U.S. PATENT AND TRADEMARK OFFICE WEBSITE. SEE BELOW:

Checker Version 3.0

The Checker Version 3.0 application is a state-of the-art Windows based software program employing a logical and intuitive user-interface to check whether a sequence listing is in compliance with format and content rules. Checker Version 3.0 works for sequence listings generated for the original version of 37 CFR §§1.821 – 1.825 effective October 1, 1990 (old rules) and the revised version (new rules) effective July 1, 1998 as well as World Intellectual Property Organization (WIPO) Standard ST.25.

Checker Version 3.0 replaces the previous DOS-based version of Checker, and is Y2K-compliant. Checker allows public users to check sequence listings in Computer Readable form (CRF) before submitting them to the United States Patent and Trademark Office (USPTO).

Use of Checker prior to filing the sequence listing is expected to result in fewer errored sequence listings, thus saving time and money.

Checker Version 3.0 can be downloaded from the USPTO website at the following address:
<http://www.uspto.gov/web/offices/pac/checker>

Raw Sequence Listing Error Summary

<u>ERROR DETECTED</u>	<u>SUGGESTED CORRECTION</u>	<u>SERIAL NUMBER:</u> <u>09/397, 957</u>
ATTN: NEW RULES CASES: PLEASE DISREGARD ENGLISH "ALPHA" HEADERS, WHICH WERE INSERTED BY PTO SOFTWARE		
1 <input type="checkbox"/> Wrapped Nucleic	The number/text at the end of each line "wrapped" down to the next line. This may occur if your file was retrieved in a word processor after creating it. Please adjust your right margin to .3, as this will prevent "wrapping".	
2 <input type="checkbox"/> Wrapped Aminos	The amino acid number/text at the end of each line "wrapped" down to the next line. This may occur if your file was retrieved in a word processor after creating it. Please adjust your right margin to .3, as this will prevent "wrapping".	
3 <input type="checkbox"/> Incorrect Line Length	The rules require that a line not exceed 72 characters in length. This includes spaces.	
4 <input type="checkbox"/> Misaligned Amino Acid Numbering	The numbering under each 5th amino acid is misaligned. This may be caused by the use of tabs between the numbering. It is recommended to delete any tabs and use spacing between the numbers.	
5 <input type="checkbox"/> Non-ASCII	This file was not saved in ASCII (DOS) text, as required by the Sequence Rules. Please ensure your subsequent submission is saved in ASCII text so that it can be processed.	
6 <input type="checkbox"/> Variable Length	Sequence(s) <input type="checkbox"/> contain n's or Xaa's which represented more than one residue. As per the rules, each n or Xaa can only represent a single residue. Please present the maximum number of each residue having variable length and indicate in the (ix) feature section that some may be missing.	
7 <input type="checkbox"/> PatentIn ver. 2.0 "bug"	A "bug" in PatentIn version 2.0 has caused the <220>-<223> section to be missing from amino acid sequence(s) <input type="checkbox"/> . Normally, PatentIn would automatically generate this section from the previously coded nucleic acid sequence. Please manually copy the relevant <220>-<223> section to the subsequent amino acid sequence. This applies primarily to the mandatory <220>-<223> sections for Artificial or Unknown sequences.	
8 <input type="checkbox"/> Skipped Sequences (OLD RULES)	Sequence(s) <input type="checkbox"/> missing. If intentional, please use the following format for each skipped sequence: (2) INFORMATION FOR SEQ ID NO:X: (i) SEQUENCE CHARACTERISTICS:(Do not insert any headings under "SEQUENCE CHARACTERISTICS") (xi) SEQUENCE DESCRIPTION:SEQ ID NO:X: This sequence is intentionally skipped Please also adjust the "(iii) NUMBER OF SEQUENCES:" response to include the skipped sequence(s).	
9 <input type="checkbox"/> Skipped Sequences (NEW RULES)	Sequence(s) <input type="checkbox"/> missing. If intentional, please use the following format for each skipped sequence. <210> sequence id number <400> sequence id number 000	
10 <input type="checkbox"/> Use of n's or Xaa's (NEW RULES)	Use of n's and/or Xaa's have been detected in the Sequence Listing. Use of <220> to <223> is MANDATORY if n's or Xaa's are present. In <220> to <223> section, please explain location of n or Xaa, and which residue n or Xaa represents.	
11 <input checked="" type="checkbox"/> Use of "Artificial" (NEW RULES)	Use of "Artificial" only as "<213> Organism" response is incomplete, per 1.823(b) of New Sequence Rules. <u>Valid response is Artificial Sequence.</u>	
12 <input type="checkbox"/> Use of <220> Feature (NEW RULES)	Sequence(s) <input type="checkbox"/> are missing the <220>Feature and associated headings. Use of <220> to <223> is MANDATORY if <213>ORGANISM is "Artificial Sequence" or "Unknown" Please explain source of genetic material in <220> to <223> section. (See "Federal Register," 6/01/98, Vol. 63, No. 104, pp. 29631-32) (Sec. 1.823 of new Rules)	
13 <input type="checkbox"/> PatentIn ver. 2.0 "bug"	Please do not use "Copy to Disk" function of PatentIn version 2.0. This causes a corrupted file, resulting in missing mandatory numeric identifiers and responses (as indicated on raw sequence listing). Instead, please use "File Manager" or any other means to copy file to floppy disk.	

RAW SEQUENCE LISTING

PATENT APPLICATION: US/09/397,957

DATE: 04/17/2001

TIME: 13:04:41

Input Set : A:\A65686-1.ST25.txt
 Output Set: N:\CRF3\04172001\I397957.raw

```

3 <110> APPLICANT: Duong, Hau
4      Kayyem, Jon
5      O'Connor, Stephen
6      Terbrueggen, Robert
8 <120> TITLE OF INVENTION: Signal Detection Techniques for the Detection of Analytes
10 <130> FILE REFERENCE: A-65686-1/RFT/RMS/RMK
12 <140> CURRENT APPLICATION NUMBER: US 09/397,957
13 <141> CURRENT FILING DATE: 1999-09-17
15 <150> PRIOR APPLICATION NUMBER: US 60/100,730
16 <151> PRIOR FILING DATE: 1998-09-17
18 <160> NUMBER OF SEQ ID NOS: 7
20 <170> SOFTWARE: PatentIn version 3.0
22 <210> SEQ ID NO: 1
23 <211> LENGTH: 15
24 <212> TYPE: DNA
C--> 25 <213> ORGANISM: Artificial
27 <220> FEATURE:
28 <223> OTHER INFORMATION: synthetic DNA target.
30 <400> SEQUENCE: 1
31 accatggaca cagat
34 <210> SEQ ID NO: 2
35 <211> LENGTH: 22
36 <212> TYPE: DNA
C--> 37 <213> ORGANISM: Artificial
39 <220> FEATURE:
40 <223> OTHER INFORMATION: synthetic DNA target.
42 <400> SEQUENCE: 2
43 tcatttgatgg tctcttttaa ca
46 <210> SEQ ID NO: 3
47 <211> LENGTH: 32
48 <212> TYPE: DNA
C--> 49 <213> ORGANISM: Artificial
51 <220> FEATURE:
52 <223> OTHER INFORMATION: synthetic DNA target.
54 <400> SEQUENCE: 3
55 cacagtgggg ggacatcaag cagccatgca aa
58 <210> SEQ ID NO: 4
59 <211> LENGTH: 18
60 <212> TYPE: DNA
C--> 61 <213> ORGANISM Artificial
63 <220> FEATURE:
64 <223> OTHER INFORMATION: synthetic DNA target.
66 <400> SEQUENCE: 4
67 tgtgcaggatc acgtggat
70 <210> SEQ ID NO: 5
71 <211> LENGTH: 72
72 <212> TYPE: DNA

```

Does Not Comply
 Corrected Diskette Needed
 pp. 1-2

Incomplete response for
<213> as per section 1.823b
of the new²² sequence rules.
See #11 on the Error
Summary Sheet.

15

32

18

RAW SEQUENCE LISTING
PATENT APPLICATION: US/09/397,957

DATE: 04/17/2001
TIME: 13:04:41

Input Set : A:\A65686-1.ST25.txt
Output Set: N:\CRF3\04172001\I397957.raw

C--> 73 <213> ORGANISM: Artificial
75 <220> FEATURE:
76 <223> OTHER INFORMATION: synthetic DNA target.
78 <400> SEQUENCE: 5
79 tgcgttgtt acgtggattt taaaagaga ccatcaatga ggaagctgca gaatggata 60
81 gagtcatcca gt 72
84 <210> SEQ ID NO: 6
85 <211> LENGTH: 23
86 <212> TYPE: DNA
C--> 87 <213> ORGANISM: Artificial
89 <220> FEATURE:
90 <223> OTHER INFORMATION: synthetic DNA target.
92 <400> SEQUENCE: 6
93 tctacagcat ctgtgtccat ggt 23
96 <210> SEQ ID NO: 7
97 <211> LENGTH: 18
98 <212> TYPE: DNA
C--> 99 <213> ORGANISM: Artificial
101 <220> FEATURE:
102 <223> OTHER INFORMATION: signal probe.
104 <400> SEQUENCE: 7
105 atccacgtca actgcaca 18

Refer to p. 1

VERIFICATION SUMMARY

PATENT APPLICATION: US/09/397,957

DATE: 04/17/2001

TIME: 13:04:42

Input Set : A:\A65686-1.ST25.txt

Output Set: N:\CRF3\04172001\I397957.raw

L:25 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:1
L:37 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:2
L:49 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:3
L:61 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:4
L:73 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:5
L:87 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:6
L:99 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:7